

CLEAN COPY OF THE AMENDED AND NEW CLAIMS

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10. (Amended) A transformed Coryneform bacterium comprising an isolated sigH gene having the polynucleotide sequence of SEQ ID NO: 1.

Please add the following new claims:

32. (New) The bacterium of claim 10, wherein said sigH gene is over-expressed.

33. (New) A transformed recombinant coryneform bacterium comprising an increased intracellular concentration or activity of polypeptide having the amino acid sequence of SEQ ID NO: 2, wherein said intracellular concentration or activity is increased by at least 10% over a concentration or activity of a wild type coryneform bacterium.

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34. (New) The coryneform bacterium of claim 33, wherein said intracellular concentration or activity is increased by at least 25 % over the concentration or activity of a wild type coryneform bacterium.

35. (New) The coryneform bacterium of claim 33, wherein said intracellular concentration or activity is increased by at least 50 % over the concentration or activity of a wild type coryneform bacterium.

36. (New) The coryneform bacterium of claim 33, wherein said polypeptide is encoded by an isolated polynucleotide comprising the nucleotide sequence of SEQ ID NO: 1 and said polypeptide is over-expressed.

37. (New) The coryneform bacterium of claim 36, wherein said isolated polynucleotide includes nucleotides 302 to 919 of SEQ ID NO: 1.

38. (New) A transformed coryneform bacterium comprising an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO: 2.

39. (New) The coryneform bacterium of claim 38, wherein said polypeptide is over-expressed to the extent that an intracellular concentration of said polypeptide is increased by at least 10% over a concentration in a wild type coryneform bacterium.

40. (New) The coryneform bacterium of claim 39, wherein said over-expression of said polypeptide is achieved by increasing the copy number of the polynucleotide encoding said polypeptide.

41. (New) The coryneform bacterium of claim 33, wherein said coryneform bacterium is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium thermoaminogenes*, *Corynebacterium melassecola*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

42. (New) The coryneform bacterium of claim 38 wherein said coryneform bacterium is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium thermoaminogenes*, *Corynebacterium melassecola*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

43. (New) The coryneform bacterium of claim 33, wherein said coryneform bacterium produces an L-amino acid selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

44. (New) The coryneform bacterium of claim 43, wherein said L-amino acid is L-lysine.

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45. (New) The coryneform bacterium of claim 34, wherein said coryneform bacterium produces an L-amino acid selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

46. (New) The coryneform bacterium of claim 45, wherein said L-amino acid is L-lysine.

47. (New) The coryneform bacterium of claim 41, wherein said coryneform bacterium produces an L-amino acid selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

48. (New) The coryneform bacterium of claim 47, wherein said L-amino acid is L-lysine.

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49. (New) A transformed coryneform bacterium comprising an over-expressed sigH gene, wherein said sigH gene comprises the nucleotide sequence of SEQ ID NO: 1.
